FIGURE 1

FIGURE 1

FIGURE 2

```
Met Asp Ile Leu Cys Glu Glu Asn Thr Ser
ATG GAT ATT CTT TGT GAA GAA ATA CTT CT
        10          20          30

Leu Ser Ser Thr Thr Asn Ser Leu Met Gln
TTG AGC TCA ACT ACG AAC TCC CTA ATG CAA
        40          50          60

Leu Asn Asp Asp Thr Arg Leu Tyr Ser Asn
TTA AAT GAT GAC ACC AGG CTC TAC AGT AAT
        70          80          90

Asp Phe Asn Ser Gly Glu Ala Asn Thr Ser
GAC TTT AAC TCC GGA GAA GCT AAC ACT TCT
        100         110         120

Asp Ala Phe Asn Trp Thr Val Asp Ser Glu
GAT GCA TTT AAC TGG ACA GTC GAC TCT GAA
        130         140         150

Asn Arg Thr Asn Leu Ser Cys Glu Gly Cys
AAT CGA ACC AAC CTT TCC TGT GAA GGG TGC
        160         170         180
```

FIGURE 2 (cont.)

```
Leu   Ser   Pro   Ser   Cys   Leu   Ser   Leu   Leu   His
C T C T C A C C G T C G T G T C T C T C C T T A C T T C A T
              190                     200                     210


Leu   Gln   Glu   Lys   Asn   Trp   Ser   Ala   Leu   Leu
C T C C A G G A A A A A A A C T G G T C T G C T T T A C T G
              220                     230                     240


Thr   Ala   Val   Val   Ile   Ile   Leu   Thr   Ile   Ala
A C A G C C G T A G T G A T T A T T C T A A C T A T T G C T
              250                     260                     270


Gly   Asn   Ile   Leu   Val   Ile   Met   Ala   Val   Ser
G G A A A C A T A C T C G T C A T C A T G G C A G T G T C C
              280                     290                     300


Leu   Glu   Lys   Lys   Leu   Gln   Asn   Ala   Thr   Asn
C T A G A G A A A A A G C T G C A G A A T G C C A C C A A C
              310                     320                     330


Tyr   Phe   Leu   Met   Ser   Leu   Ala   Ile   Ala   Asp
T A T T T C C T G A T G T C A C T T G C C A T A G C T G A T
              340                     350                     360


Met   Leu   Leu   Gly   Phe   Leu   Val   Met   Pro   Val
A T G C T G C T G G G T T T C C T T G T C A T G C C C G T G
              370                     380                     390


Ser   Met   Leu   Thr   Ile   Leu   Tyr   Gly   Tyr   Arg
T C C A T G T T A A C C A T C C T G T A T G G G T A C C G G
              400                     410                     420
```

FIGURE 2 (cont.)

```
Trp     Pro     Leu     Pro     Ser     Lys     Leu     Cys     Ala     Val
T G G   C C T   C T G   C C G   A G C   A A G   C T T   T G T   C A G   T C
               430                             440                            450


Trp     Ile     Tyr     Leu     Asp     Val     Leu     Phe     Ser     Thr
T G G   A T T   T A C   C T G   G A C   G T G   C T C   T T C   T C C   A C G
               460                             470                            480


Ala     Ser     Ile     Met     His     Leu     Cys     Ala     Ile     Ser
G C C   T C C   A T C   A T G   C A C   C T C   T G C   G C C   A T C   T C G
               490                             500                            510


Leu     Asp     Arg     Tyr     Val     Ala     Ile     Gln     Asn     Pro
C T G   G A C   C G C   T A C   G T C   G C C   A T C   C A G   A A T   C C C
               520                             530                            540


Ile     His     His     Ser     Arg     Phe     Asn     Ser     Arg     Thr
A T C   C A C   C A C   A G C   C G C   T T C   A A C   T C C   A G A   A C T
               550                             560                            570


Lys     Ala     Phe     Leu     Lys     Ile     Ile     Ala     Val     Trp
A A G   G C A   T T T   C T G   A A A   A T C   A T T   G C T   G T T   G G
               580                             590                            600


Thr     Ile     Ser     Val     Gly     Ile     Ser     Met     Pro     Ile
A C C   A T A   T C A   G T A   G G T   A T A   T C C   A T G   C C A   A T A
               610                             620                            630


Pro     Val     Phe     Gly     Leu     Gln     Asp     Asp     Ser     Lys
C C A   G T C   T T T   G G G   C T A   C A G   G A C   G A T   T C G   A A G
               640                             650                            660
```

FIGURE 2 (cont.)

```
Val   Phe   Lys   Glu   Gly   Ser   Cys   Leu   Leu   Ala
G T C T T T A A G G A G G G G A G T T G C T T A C T T G C C
            670                 680                 690


Asp   Asp   Asn   Phe   Val   Leu   Ile   Gly   Ser   Phe
G A T G A T A A C T T T G T C C T G A T C G G C T C T T T
            700                 710                 720


Val   Ser   Phe   Phe   Ile   Pro   Leu   Thr   Ile   Met
G T G T C A T T T T T C A T T C C C T T A A C C A T C A T G
            730                 740                 750


Val   Ile   Thr   Tyr   Phe   Leu   Thr   Ile   Lys   Ser
G T G A T C A C C T A C T T T C T A A C T A T C A A G T C A
            760                 770                 780


Leu   Gln   Lys   Glu   Ala   Thr   Leu   Cys   Val   Ser
C T C C A G A A A G A A G C T A C T T T G T G T G T A A G T
            790                 800                 810


Asp   Leu   Gly   Thr   Arg   Ala   Lys   Leu   Ala   Ser
G A T C T T G G C A C A C G G C C A A A T T A G C T T C T
            820                 830                 840


Phe   Ser   Phe   Leu   Pro   Gln   Ser   Ser   Leu   Ser
T T C A G C T T C C T C C C T C A G A G T T C T T T G T C T
            850                 860                 870


Ser   Glu   Lys   Leu   Phe   Gln   Arg   Ser   Ile   His
T C A G A A A A G C T C T T C C A G C G G T C G A T C C A T
            880                 890                 900
```

FIGURE 2 (cont.)

```
Arg     Glu     Pro     Gly     Ser     Tyr     Thr     Gly     Arg     Arg
A G G   A G C   C A G   G G T   C C T   A C A   C A G   G C A   G G A   G G
          910                     920                     930


Thr     Met     Gln     Ser     Ile     Ser     Asn     Glu     Gln     Lys
A C T   A T G   C A G   T C C   A T C   A G C   A A T   G A G   C A A   A A G
          940                     950                     960


Ala     Cys     Lys     Val     Leu     Gly     Ile     Val     Phe     Phe
G C A   T G C   A A G   G T G   C T G   G G C   A T C   G T C   T T C   T T C
          970                     980                     990


Leu     Phe     Val     Val     Met     Trp     Cys     Pro     Phe     Phe
C T G   T T T   G T G   G T G   A T G   T G G   T G C   C C T   T T C   T T C
          1000                    1010                    1020


Ile     Thr     Asn     Ile     Met     Ala     Val     Ile     Cys     Lys
A T C   A C A   A A C   A T C   A T G   G C C   G T C   A T C   T G C   A A A
          1030                    1040                    1050


Glu     Ser     Cys     Asn     Glu     Asp     Val     Ile     Gly     Ala
G A G   T C C   T G C   A A T   G A G   G A T   G T C   A T T   G G G   C C
          1060                    1070                    1080


Leu     Leu     Asn     Val     Phe     Val     Trp     Ile     Gly     Tyr
C T G   C T C   A A T   G T G   T T T   G T T   T G G   A T C   G G T   A T
          1090                    1100-                   1110


Leu     Ser     Ser     Ala     Val     Asn     Pro     Leu     Val     Tyr
C T C   T C T   T C A   G C A   G T C   A A C   C C A   C T A   G T C   T A C
          1120                    1130                    1140
```

FIGURE 2 (cont.)

```
Thr     Leu     Phe     Asn     Lys     Thr     Tyr     Arg     Ser     Ala
A  C  A  C  T  G  T  T  C  A  A  C  A  A  G  A  C  C  T  A  T  A  G  G  T  C  A  G  C  C
              1150                            1160                            1170


Phe     Ser     Arg     Tyr     Ile     Gln     Cys     Gln     Tyr     Lys
T  T  T  T  C  A  C  G  G  T  A  T  A  T  T  C  A  G  T  G  T  C  A  G  T  A  C  A  A  G
              1180                            1190                            1200


Glu     Asn     Lys     Lys     Pro     Leu     Gln     Leu     Ile     Leu
G  A  A  A  A  C  A  A  A  A  A  A  C  C  A  T  T  G  C  A  G  T  T  A  A  T  T  T  T  A
              1210                            1220                            1230


Val     Asn     Thr     Ile     Pro     Ala     Leu     Ala     Tyr     Lys
G  T  G  A  A  C  A  C  A  A  T  A  C  C  G  G  C  T  T  T  G  G  C  C  T  A  C  A  A  G
              1240                            1250                            1260


Ser     Ser     Gln     Leu     Gln     Met     Gly     Gln     Lys     Lys
T  C  T  A  G  C  C  A  A  C  T  T  C  A  A  A  T  G  G  G  A  C  A  A  A  A  A  A  A  G
              1270                            1280                            1290


Asn     Ser     Lys     Gln     Asp     Ala     Lys     Thr     Thr     Asp
A  A  T  T  C  A  A  A  G  C  A  A  G  A  T  G  C  C  A  A  G  A  C  A  A  C  A  G  A  T
              1300                            1310                            1320


Asn     Asp     Cys     Ser     Met     Val     Ala     Leu     Gly     Lys
A  A  T  G  A  C  T  G  C  T  C  A  A  T  G  G  T  T  G  C  T  C  T  A  G  G  A  A  A  G
              1330                            1340                            1350


Gln     His     Ser     Glu     Glu     Ala     Ser     Lys     Asp     Asn
C  A  G  C  A  T  T  C  T  G  A  A  G  A  G  G  C  T  T  C  T  A  A  A  G  A  C  A  A  T
              1360                            1370                            1380
```
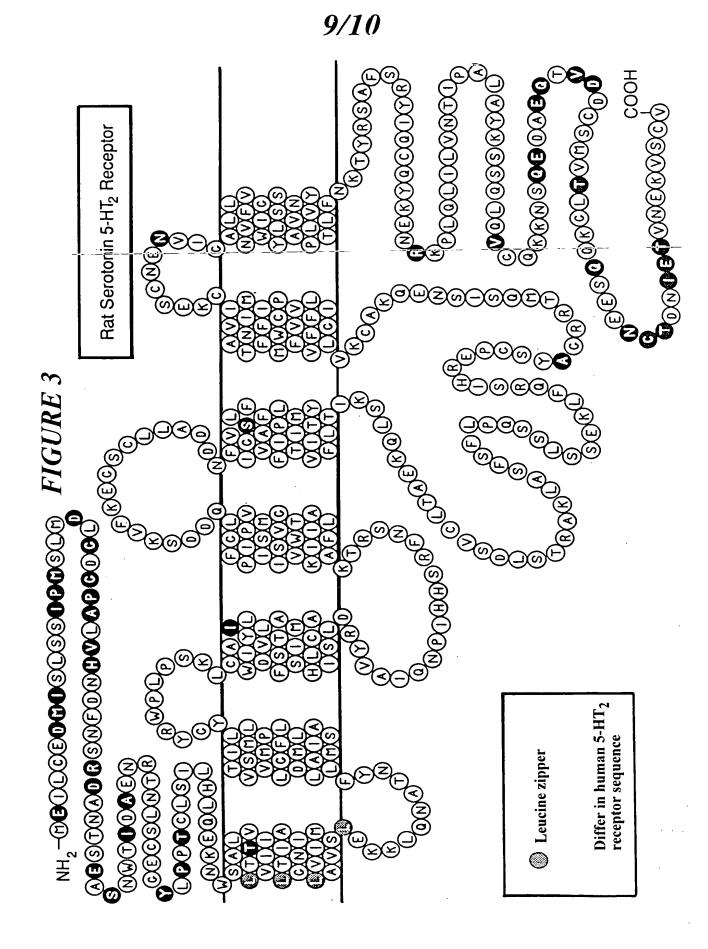
FIGURE 2 (cont.)

Ser Asp Gly Val Asn Glu Lys Val Ser Cys
AGCGACGGAGTGAATGAAAAGGTGAGCTGT
        1390   1400   1410

Val *** *** Ala Ser Cys Arg Gly Asn Cys
GTGTGATAGGCTAGTTGCCGTGGCAACTGT
        1420   1430   1440

GGAAGGCACACTGAGCAAGTTTCACCTAT
        1450   1460   1470

CTGGTTTTTTTG
        1480

FIGURE 3

Rat Serotonin 5-HT₂ Receptor

Leucine zipper

Differ in human 5-HT₂ receptor sequence

FIGURE 4

FIGURE 4. Graph of Pmols/mg protein versus ^{3}H-KETANSERIN (nM), showing $K_D = 0.68$ nM and $B_{max} = 0.61$ pmol/mg prot.